AMENDMENT

IN THE SPECIFICATION:

A. On page 1, please amend the title of the instant application to:

NUCLEIC ACID MOLECULE ENCODING CHEMOKINE-LIKE FACTOR 1 (CKLF1)

B. On page 9, please amend the third paragraph to:

The deposits(s) referred to herein will be maintained at the China Committee For Culture Collection of Microorganisms, General Microbiological Culture Center, Zhongguancun, Beijing, China 100080 (Name and Address of Depository) under the terms of the Budapest Treaty on the International Recognition of the Deposit of Microorganisms for purposes of Patent Procedure. These deposits are "provided" merely as a convenience to those skill in the art and are not an admission that a deposit is required under 35 U.S.C. §112. The sequence of the polynucleotides contained in the deposited materials, as well as reference and are controlling in the event of any conflict with any description of sequences herein. A license may be required to make, use or sell the deposited materials, and no such license is hereby granted.

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C. On page 22, please amend the paragraph prior to the last paragraph to:

The DNA sequence is shown in SEQ ID NO: 1. The encoding sequence was assembled by overlapping ESTs (Express Sequence Tags) provided by the EST Assembly Machine. The accession number of EST fragments used for the CKLF1 assembly were W38899, N95062., AA429945, AA987264, AA927461, W19056, N89912, AA516431, AA479657, AA455042, AA989129, W52820. The obtained full-length cDNA of CKLF1 has 534 base pair nucleotides, including a poly(A) tail and a polyadenylation signal ATTAAA. The open reading frame of CKLF1 is from nucleotide

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152 to nucleotide 448 as showed in SEQ ID NO:1, which encodes a polypeptide which has 99 amino acid residues. The homology analysis was conducted through GenBank on World Wide Web. The GenBank access (registration) number of CKLF1 is AF096895.

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D. On page 22, please amend the last paragraph to:

The characteristics of CKLF1 amino acid (as set forth in SEQ ID NO: 2) were analyzed with softwares PcGene, Prosite and Signal P server provided by the World Wide Web site. The result shows there is a CC motif in CKLF1 amino acid, which is characteristic of the C--C chemokine subfamily. The first amino acid residue of the deduced mature polypeptide is glycine. The deduced CKLF1 protein has no typical signal cleavage site, no transmembrane domain, no DNA binding site and no putative N-glycosylation site. The first 17 amino acid residues of the N-terminal are hydrophobic and are the possible signal peptide. The homology analysis showed that the CKLF1 polypeptide shares no obvious homology with known proteins; amino acid 35 through 79 shares 46 percent homology with the permease of Caenorhabditis elegans.

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E. On page 23, please amend the second paragraph to:

The 5' oligonucleotide primer 1 (P1, SEQ ID NO: 9) and 3'oligonucleotide primer 2 (P2, SEQ ID NO: 10) were designed according to the coding sequence of the CKLF1 polynucleotide. The sequences are shown as follows: P1, SEQ ID NO: 9: 5'ATG GAT AAC GTG CAG CCG AAA AT 3', P2, SEQ ID NO: 10: 5'CCG CTC GAG TTA CAA AAC TTC TTT TTT TTC 3'.

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F. On page 24, please amend the paragraph prior to the last paragraph to:

The 5' oligonucleotide primer 1' (P1', SEQ ID NO: 11) and the 3' oligonucleotide primer 2' (P2', SEQ ID NO: 12) were designed according to the cDNA sequence of

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CKLF1. The 3' primer contains a complementary sequence to the XhoII site. The primers are as follows:

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P1', SEQ ID NO: 11: 5'CTG ATA CCA GAA ACC ACA ACA TT 3'

P2', SEQ ID NO: 12: 5'GGA AGA ATA CAG AAA TAT GTT TAA TAC 3'

G. On page 25, please amend the paragraph prior to the last paragraph to:

The coding regions of CKLF1, 2 and 4 were amplified by using primer 1 (P1) and primer 5 (P5, SEQ ID NO: 13: 5' CGG GAT CCA AAA CTT CTT TTT TTT CAT GC 3'). In the coding region of CKLF1, 2 and 4, the stop codon was removed and a BamHI site was introduced near the 3' end. The PCR products were blunted by klenow enzyme and then digested with BamHI. The pEGFP-N1 expression vector (CLOTECH) was digested with EcoRI, blunted with klenow enzyme and then digested with BamHI. After purification and recovery from the agarose gels, the fragments were ligated into the digested vectors. The recombinant plasmids were designated pEGFP-CKLF1, 2 and 4, respectively. The coding sequences of CKLF1, 2 and 4 were the same as the open reading frame of EGFP.

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IN THE CLAIMS:

A. Kindly withdraw Claims 6-8, 11-13 and 17-33, without prejudice, as drawn to a non-elected group invention. The remaining pending claims are 1-5, 9-10 and 14-16.

B. To facilitate examination of the remaining pending claims, Applicants cancel remaining pending claims 1-5, 9-10 and 14-16, without prejudice, in favor of new claims 34 through 72. Please note that new Claim 34 corresponds to portions of cancelled pending Claim 1 (Claim 1a and 1b), new Claim 51 corresponds to a portion of cancelled pending Claim 1 (Claim 1g), new Claim 64 corresponds to portions of cancelled pending Claim 1 (Claim 1f and 1h), and the remaining new claims are comparable in scope with the other cancelled pending claims.